




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#11 Search **BRCA2 fusion protein**

11:48:00 22

#10 Search **RAD51 fusion protein**

11:47:26 74

#7 Search **#5 and structure**

11:47:08 9

#9 Search **fds**

11:45:52 404

#6 Search **#5 and crystal and structure**

09:31:29 2

#5 Search **RAD51-BRC**

09:31:15 31

#2 Search **#1 and crystal**

09:17:51 2

#1 Search **RAD51 and BRC**

09:17:08 31

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		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L5	RAD51 and (venkitaraman\$ or pellegrini\$ or blundell\$ or yu\$ or bates\$).in.	18
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<input type="checkbox"/>	L3	L1 and "crystal".clm.	0
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<input type="checkbox"/>	L1	RAD51 and BRCA	40

END OF SEARCH HISTORY

STN

10531242

=> d his

(FILE 'HOME' ENTERED AT 13:04:12 ON 13 JUN 2007)

FILE 'CAPLUS' ENTERED AT 13:04:53 ON 13 JUN 2007

L1 34 S RAD51 AND BRC

L2 4 S L1 AND CRYSTAL

=> d L2 1-4

L2 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2004:354973 CAPLUS

DN 140:334412

TI Use of crystal structure of human RAD51-BRCA2
BRC repeat complex in screening for anti tumor agents

IN Venkitaraman, Ashok; Pellegrini, Luca; Blundell, Tom; Yu, David; Lo,
Thomas; Bates, Debbie; Shivji, Mahmud; Anand, Shubha; Lee, Miyoung

PA Cambridge University Technical Services Ltd., UK

SO PCT Int. Appl., 102 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2004035621	A2	20040429	WO 2003-GB4485	20031014
	WO 2004035621	A3	20040826		
	AU 2003271967	A1	20040504	AU 2003-271967	20031014
	EP 1551871	A2	20050713	EP 2003-753806	20031014
	EP 1650223	A2	20060426	EP 2005-26068	20031014
	EP 1650223	A3	20060726		
	US 2006234293	A1	20061019	US 2005-531242	20050524
PRAI	GB 2002-23860	A	20021014		
	EP 2003-753806	A3	20031014		
	WO 2003-GB4485	W	20031014		

L2 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:705265 CAPLUS

DN 140:72789

TI Sequence fingerprints in BRCA2 and RAD51: implications for DNA
repair and cancer

AU Lo, Thomas; Pellegrini, Luca; Venkitaraman, Ashok R.; Blundell, Tom L.

CS Department of Biochemistry, University of Cambridge, Cambridge, CB2 1GA,
UK

SO DNA Repair (2003), 2(9), 1015-1028

CODEN: DRNEAR; ISSN: 1568-7864

PB Elsevier Science B.V.

DT Journal

LA English

RE.CNT 61. THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN

AN 2003:681788 CAPLUS

DN 139:318901

TI Full-length archaeal Rad51 structure and mutants: mechanisms for
RAD51 assembly and control by BRCA2

AU Shin, David S.; Pellegrini, Luca; Daniels, Douglas S.; Yelent, Biana;
Craig, Lisa; Bates, Debbie; Yu, David S.; Shivji, Mahmud K.; Hitomi,
Chiharu; Arvai, Andrew S.; Volkmann, Niels; Tsuruta, Hiro; Blundell, Tom

L.; Venkitaraman, Ashok R.; Tainer, John A.
CS Department of Molecular Biology and The Skaggs Institute for Chemical
Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA
SO EMBO Journal (2003), 22(17), 4566-4576
CODEN: EMJODG; ISSN: 0261-4189
PB Oxford University Press
DT Journal
LA English

RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2007 ACS on STN
AN 2002:883768 CAPLUS
DN 138:200905
TI Insights into DNA recombination from the structure of a RAD51
-BRCA2 complex
AU Pellegrini, Luca; Yu, David S.; Lo, Thomas; Anand, Shubha; Lee, MiYoung;
Blundell, Tom L.; Venkitaraman, Ashok R.
CS Department of Biochemistry, University of Cambridge, Cambridge, CB2 1GA,
UK
SO Nature (London, United Kingdom) (2002), 420(6913), 287-293
CODEN: NATUAS; ISSN: 0028-0836
PB Nature Publishing Group
DT Journal
LA English

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
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 ☒ Author

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1n0w

DOI 10.2210/pdb1n0w/pdb

Images and Videos

Biological Molecules

Red - Derived Information

Title Crystal structure of a RAD51-BRCA2
BRC repeat complex

Authors Pellegrini, L., Yu, D.S., Lo,
T., Anand, S., Lee, M., Blundell,
T.L., Venkitaraman, A.R.
Primary Citation
 Pellegrini, L., Yu, D.S., Lo, T., Anand,
S., Lee, M., Blundell,
T.L., Venkitaraman, A.R. Insights into
DNA recombination from the structure of a
RAD51-BRCA2 complex *Nature* v420
pp.287-293, 2002

[Abstract]

History
 Deposition 2002-10-15 Release 2002-
11-27
Experimental Method
 Type X-RAY DIFFRACTION Data
[EDS]
Parameters

Resolution [Å]	R-Value	R-Free	Space Group
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Unit Cell

Length [Å]	a	b	c
57.30	59.14	77.20	

Angles [°]	alpha	beta	gamma
90.00	90.00	90.00	

Molecular Description
Asymmetric Unit

 Polymer: 1 Molecule: DNA repair protein
RAD51 homolog 1 Fragment: ATPase
domain Chains: A
 Polymer: 2 Molecule: Breast cancer type 2
susceptibility protein Fragment: BRC
repeat type 4 Chains: B
 Polymer: 3 Molecule: peptide linker
Chains: L Other Details: this peptide links
the BRCA2 to the RAD51
 Polymer: 4 Molecule: ARTIFICIAL GLY-
SER-MSE-GLY PEPTIDE Chains: C
 Other Details: this peptide comes from the
expression vector and is linked to the N-
terminus of BRCA2

■ 1N0W

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Structure Analysis

Help

 To view the 3D structure
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Display

MBT Pi

Classification Gene Regulation/antitumor Protein

Source

Polymer: 1 Scientific Name: **Homo sapiens** Common Name: **Human**
 Polymer: 2 Scientific Name: **Escherichia coli** Common Name: **Escherichia coli**
 Expression system: **Escherichia coli**
 Unknown Expression system: **Escherichia coli**
 Unknown Expression system: **Escherichia coli**

Chemical Component

Identifier Name	Formula	Drug Similarity	He
MSE SELENOMETHIONINE	$C_5 H_{11} N O_2$ Se		
MG MAGNESIUM ION	Mg^{2+}		
EDO 1,2-ETHANEDIOL	$C_2 H_6 O_2$		
CL CHLORIDE ION	Cl^-		

SCOP Classification (version 1.71)

Domain Info	Class	Fold	Superfamily	Family
d1n0wa_	Alpha and beta proteins (a/b)	P-loop containing nucleoside triphosphate hydrolases	P-loop containing nucleoside triphosphate hydrolases	RecA protein-like (ATPase-domain)
d1n0wb_	Peptides	BRCA2 BRC4 repeat	BRCA2 BRC4 repeat	BRCA2 BRC4 repeat

CATH Classification (version v3.0.0)

Domain	Class	Architecture	Topology
1n0wA00	Alpha Beta	3-Layer(aba) Sandwich	Rossmann

PFAM Classification

Chain	PFAM Accession	PFAM ID	Description	Type
A	PF08423	Rad51	Rad51	Dom
B	PF00634	BRCA2	BRCA2 repeat	Fam

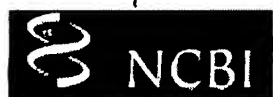
GO Terms

Polymer	Molecular Function	Biological Process
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Breast cancer type 2
susceptibility protein
(1N0W:B)
peptide linker (1N0W:L)
ARTIFICIAL GLY-SER-
MSE-GLY PEPTIDE
(1N0W:C)

- activity
- nucleoside-triphosphatase activity
- nucleoside-triphosphatase activity

- none
- DNA repair
- DNA repair
- none
- none



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☐ 1: [P42212](#). Reports Green fluorescent...[gi:1169893]BLink, Conserved
Domains, Links[Comment](#) [Features](#) [Sequence](#)

LOCUS [P42212](#) 238 aa linear INV 01-MAY-2007

DEFINITION [Green fluorescent protein.](#)

ACCESSION [P42212](#)

VERSION [P42212](#) [GI:1169893](#)

DBSOURCE [swissprot: locus GFP_AEQVI, accession \[P42212\]\(#\);](#)
[class: standard.](#)
[extra accessions: Q17104, Q27903](#)
[created: Nov 1, 1995.](#)
[sequence updated: Nov 1, 1995.](#)
[annotation updated: May 1, 2007.](#)
[xrefs: M62654.1, AAA27722.1, M62653.1, AAA27721.1, L29345.1,](#)
[AAA58246.1, X96418.1, CAA65278.1, JQ1514, 1B9CA, 1B9CB, 1B9CC,](#)
[1B9CD, 1BFP_, 1C4FA, 1CV7A, 1EMA_, 1EMB_, 1EMCA, 1EMCB, 1EMCC,](#)
[1EMCD, 1EME_, 1EMF_, 1EMGA, 1EMK_, 1EML_, 1EMM_, 1F09A, 1F0BA,](#)
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[1HUYA, 1JBYA, 1JBZA, 1JC0A, 1JC0B, 1JC0C, 1JC1A, 1JC1B, 1JC1C,](#)
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[1RMMA, 1RMOA, 1RMPA, 1RRXA, 1W7SA, 1W7SB, 1W7SC, 1W7SD, 1W7TA,](#)
[1W7TB, 1W7TC, 1W7TD, 1W7UA, 1W7UB, 1W7UC, 1W7UD, 1YFPA, 1YFPB,](#)
[1YHGA, 1YHGB, 1YHHA, 1YHIA, 1YJ2A, 1YJFA, 1Z1PA, 1Z1QA, 2AH8A,](#)
[2AH8B, 2AHAA, 2AHAB, 2AWJA, 2AWKA, 2AWLA, 2AWMA, 2B3QA, 2B3QB,](#)
[2B3QC, 2B3QD, 2EMD_, 2EMN_, 2EMO_, 2FWQA, 2FZUA, 2G16A, 2G2SB,](#)
[2G3DA, 2G3DB, 2G5ZA, 2G5ZB, 2G6EA](#)
[xrefs \(non-sequence databases\): LinkHub:P42212, GO:0008218,](#)
[GO:0006091, InterPro:IPR009017, InterPro:IPR011584,](#)
[InterPro:IPR000786, Gene3D:G3DSA:2.40.155.10, Pfam:PF01353,](#)
[PRINTS:PR01229, ProDom:PD013756](#)

KEYWORDS 3D-structure; Chromophore; Direct protein sequencing; Luminescence;
Photoprotein.

SOURCE [Aequorea victoria](#)

ORGANISM [Aequorea victoria](#)
[Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;](#)
[Aequoreidae; Aequorea.](#)

REFERENCE 1 (residues 1 to 238)

AUTHORS Prasher,D.C., Eckenrode,V.K., Ward,W.W., Prendergast,F.G. and
Cormier,M.J.

TITLE Primary structure of the *Aequorea victoria* green-fluorescent
protein

JOURNAL [Gene](#) 111 (2), 229-233 (1992)

PUBMED [1347277](#)

REMARK NUCLEOTIDE SEQUENCE [MRNA], AND PARTIAL PROTEIN SEQUENCE.

REFERENCE 2 (residues 1 to 238)

AUTHORS Inouye,S. and Tsuji,F.I.

TITLE *Aequorea* green fluorescent protein. Expression of the gene and

fluorescence characteristics of the recombinant protein
JOURNAL FEBS Lett. 341 (2-3), 277-280 (1994)
PUBMED [8137953](#)
REMARK NUCLEOTIDE SEQUENCE [MRNA].
REFERENCE 3 (residues 1 to 238)
AUTHORS Rouwendal, G.J., Mendes, O., Wolbert, E.J. and Douwe de Boer, A.
TITLE Enhanced expression in tobacco of the gene encoding green
fluorescent protein by modification of its codon usage
JOURNAL Plant Mol. Biol. 33 (6), 989-999 (1997)
PUBMED [9154981](#)
REMARK NUCLEOTIDE SEQUENCE [MRNA].
REFERENCE 4 (residues 1 to 238)
AUTHORS Cody, C.W., Prasher, D.C., Westler, W.M., Prendergast, F.G. and
Ward, W.W.
TITLE Chemical structure of the hexapeptide chromophore of the Aequorea
green-fluorescent protein
JOURNAL Biochemistry 32 (5), 1212-1218 (1993)
PUBMED [8448132](#)
REMARK CHROMOPHORE.
REFERENCE 5 (residues 1 to 238)
AUTHORS Ormo, M., Cubitt, A.B., Kallio, K., Gross, L.A., Tsien, R.Y. and
Remington, S.J.
TITLE Crystal structure of the Aequorea victoria green fluorescent
protein
JOURNAL Science 273 (5280), 1392-1395 (1996)
PUBMED [8703075](#)
REMARK X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
REFERENCE 6 (residues 1 to 238)
AUTHORS Yang, F., Moss, L.G. and Phillips, G.N. Jr.
TITLE The molecular structure of green fluorescent protein
JOURNAL Nat. Biotechnol. 14 (10), 1246-1251 (1996)
PUBMED [9631087](#)
REMARK X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
REFERENCE 7 (residues 1 to 238)
AUTHORS Wachter, R.M., Elsliger, M.A., Kallio, K., Hanson, G.T. and
Remington, S.J.
TITLE Structural basis of spectral shifts in the yellow-emission variants
of green fluorescent protein
JOURNAL Structure 6 (10), 1267-1277 (1998)
PUBMED [9782051](#)
REMARK X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF MUTANT WITH YELLOW
EMISSION.
REFERENCE 8 (residues 1 to 238)
AUTHORS Elsliger, M.A., Wachter, R.M., Hanson, G.T., Kallio, K. and
Remington, S.J.
TITLE Structural and spectral response of green fluorescent protein
variants to changes in pH
JOURNAL Biochemistry 38 (17), 5296-5301 (1999)
PUBMED [10220315](#)
REMARK X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
COMMENT On Apr 26, 2005 this sequence version replaced [gi:7428731](#).
[FUNCTION] Energy-transfer acceptor. Its role is to transduce the
blue chemiluminescence of the protein aequorin into green
fluorescent light by energy transfer. Fluoresces in vivo upon
receiving energy from the Ca(2+)-activated photoprotein aequorin.
[BIOPHYSICOCHEMICAL PROPERTIES] Absorption: Abs(max)=395 nm;
Note=Exhibits a smaller absorbance peak at 470 nm. The fluorescence
emission spectrum peaks at 509 nm with a shoulder at 540 nm.
[SUBUNIT] Monomer.
[TISSUE SPECIFICITY] Photocytes.
[PTM] Contains a chromophore consisting of modified amino acid
residues. The chromophore is formed by autocatalytic backbone
condensation between Xaa-N and Gly-(N+2), and oxidation of

Tyr-(N+1) to didehydrotyrosine. Maturation of the chromophore requires nothing other than molecular oxygen.

[BIOTECHNOLOGY] Fluorescent proteins have become a useful and ubiquitous tool for making chimeric proteins, where they function as a fluorescent protein tag. Typically they tolerate N- and C-terminal fusion to a broad variety of proteins. They have been expressed in most known cell types and are used as a noninvasive fluorescent marker in living cells and organisms. They enable a wide range of applications where they have functioned as a cell lineage tracer, reporter of gene expression, or as a measure of protein-protein interactions.

[SIMILARITY] Belongs to the GFP family.

[WEB RESOURCE] NAME=Protein Spotlight; NOTE=The greenest of us all - Issue 11 of June 2001;

URL=http://www.expasy.org/spotlight/back_issues/sptlt011.shtml'.

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121 nriélkgidf kedgnilghk leynynshnv yimadkqkng ikvnfkihrn iedgsvqlad
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//

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☐ 1: CAA64484, Reports brca2 [Homo sapie...[gi:1177438]BLink, Conserved
Domains, LinksFeatures Sequence

LOCUS CAA64484 3418 aa linear PRI 14-NOV-2006

DEFINITION brca2 [Homo sapiens].

ACCESSION CAA64484

VERSION CAA64484.1 GI:1177438

DBSOURCE embl accession X95152.1embl accession X95153.1embl accession X95154.1embl accession X95155.1embl accession X95156.1embl accession X95157.1embl accession X95158.1embl accession X95159.1embl accession X95160.1embl accession X95161.1embl accession X95162.1embl accession X95163.1embl accession X95164.1embl accession X95165.1embl accession X95166.1embl accession X95167.1embl accession X95168.1embl accession X95169.1embl accession X95170.1embl accession X95171.1embl accession X95172.1embl accession X95173.1embl accession X95174.1embl accession X95175.1embl accession X95176.1embl accession X95177.1

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiensEukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS

Wooster,R., Bignell,G., Lancaster,J., Swift,S., Seal,S.,
Mangion,J., Collins,N., Gregory,S., Gumbs,C., Micklem,G.,
Barfoot,R., Hamoudi,R., Patel,S., Rice,C., Biggs,P., Hashim,Y.,
Smith,A., Connor,F., Arason,A., Gudmundsson,J., Ficenece,D.,
Kelsell,D., Ford,D., Tonin,P., Bishop,D.T., Spurr,N.K.,
Ponder,B.A.J., Eeles,R., Peto,J., Devilee,P., Cornelisse,C.,
Lynch,H., Narod,S., Lenoir,G., Egilsson,V., Barkadottir,R.B.,
Easton,D.F., Bentley,D.R., Futreal,P.A., Ashworth,A. and

Stratton,M.R.
TITLE Identification of the breast cancer susceptibility gene BRCA2
JOURNAL Nature 378 (6559), 789-792 (1995)
PUBMED 8524414
REMARK Erratum: [Nature 1996 Feb 22;379(6567):749]
REFERENCE 2 (residues 1 to 3418)
AUTHORS Wooster,R.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1996) R. Wooster, Institute of Cancer Research,
Haddow Labs, 15 Cotswold Rd, Sutton, Surrey, SM2 5NG, UK

FEATURES Location/Qualifiers
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/chromosome="13"
/map="13q"
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(alpha 1, alpha 8, alpha 9, alpha 10) and two successive
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/db_xref="CDD:72965"

Region

2814..3054

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C-terminal ssDNA binding domain (DBD) of BRCA2 (breast cancer susceptibility gene 2) protein, called BRCA2DBD; cd04494"

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Region

3073..3167

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C-terminal ssDNA binding domain (DBD) of BRCA2 (breast cancer susceptibility gene 2) protein, called BRCA2DBD; cd04495"

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/db_xref="GOA:P51587"

/db_xref="HGNC:1101"

/db_xref="PDB:1NOW"

/db_xref="UniProtKB/Swiss-Prot:P51587"

ORIGIN

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121 ktkmdqaddv scpllncs espvvlqcth vtpqrdksvv cgslfhtpkf vkgrqtpkhi
181 seslgaevdp dmswssslat pptlsstvli vrneeasetv fphdttanvk syfsnhdesl
241 kkndrfiasv tdsentnqre aashgfgkts gnsfkvnsc dhigksmpnv ledevyetvv
301 dtseedsfsl cfskcrtnl qkvrtsktrk kifheanade ceksknqvke kysfvsevep
361 ndtdpldsnv anqkpfesgs dkiskevps lacewsqtl1 sglngaqmek iqlhisscd
421 qnisekdldd tenkrkkdfl tsenslpris slpksekpln eetvvnkrde eqhleshtdc
481 ilavkqaisg tspvassfgg ikksifrire spketfnasf sghmtdpnfk keteasesgl
541 eihtvcsqke dslcpnlidn gswpatattqn svalknagli stlkkktnkf iyaihketsy
601 kgkkipkdqk selincsaqf eanafeaplt fanadsgllh ssvkrscsqn dseepthlt
661 ssfgtilrkc srnetcsnt visqdldyke akcnkeklql fitpeadsls clqegqcxnd
721 pkskkvsdik eevlaaachp vqhskevysd tdfqsqknll ydhenastli ltpstkdvl
781 nlvmisrgke sykmsdklkg nnyesdvlt knipmeknqd vcalnenykn vellppekym
841 rvaspsrvkvq fnqntnlrvi qknqeetst1 skitvnpdse elfsdnennf vfgvanern
901 lalntkelh etdltcvnep ifknstmvly gdtgdkqatq vsikkdlvyv laenknsvk
961 qhikmtlgqd lksdislnid kipeknndym nkagllgpi snhsfggsfr tasnkeikls
1021 ehnikkskmf fkdieeqypt slacveivnt laldnqkkl kppsintvsa hlgssvvvsd
1081 cknshitpqn lfskqdfnsn hnltspqkae itelstilee sgsgfeftqf rkpsylqks
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1201 nksasgyltd enevgfrgfy sahgtklvns tealqkavkl fsdienisee tsaevhplsl
1261 ssskchdsdv smfkienhnd ktvseknnkc qlilqnniem ttgtfveeit enykrntene
1321 dnkytaasrn shnlefdgsd sskndtvcih kdetdlldf qhniclklsg qfmkegntqi
1381 kedlsdltfl evakaqeach gntsnkeqlt atkteqnikd fetsdtffqt asgknisvak
1441 esfnkivnff dqkpeelhnd slnselhsdi rknkmdilsy eetdivkhki lkesvpvgtg

Repeated Sequence

• 1501 nqlvtfggqp erdekikept llgfhtasgk kvkiakesld kvknlfdeke qgtseitsfs
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1621 crqtenlktks ksiflkvkvh enveketaks patcytnqsp ysviensala fytscsrkts
1681 vsqtslleak kwlregifdg qperintady vgnlyyenns nstiaendkn hlsekqdtlyl
1741 snssmsnsys yhsdevynds rilsknndls giepvlnve dqkntsfskv isnvkdanay
1801 pqtvnedicv eeltvssspc knknaaikls isnsnnfevg ppafriasgk ivcvshetik
1861 kvkdiftdsf skvikennen kskicqtkim agcyealdds edilhnsldn decsthshkv
1921 fadiqseeil qhnqnmgle kvskispcdv sletsdickc sigklhksvs santcgifst
1981 asgksqvgsd aslqnarqv seiedstkqv fskvlfksne hsdqltreen tairtpehli
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2161 dkqqlvlgtk vslvenihvl gkeqaspkv kmeigktetf sdvpvktne vcostyskdse
2221 nyfeteavei akafmeddel tdsklpshat hslftcpene xmvlnsrig krrgeplilv
2281 gepsikrnl nefdr¹ienq ekslkaskst pdgtikdril fmhhvslepi tcvpfrttke
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2581 ladggwlips ndgkagkeef yralcdtpgv dpklisriwv ynhyrwiwk laamecafpk
2641 efanrclspe rvllqlkyry dteidrsrrs aikkimerdd taaktvlcv sdiislsani
2701 setssnktss adtqkvaie ltdgwyavka qldppllav kngrltvqgk iilhgaelv
2761 spdactplea peslmlkisa nstrparwy klgffpdprp fplplsslfs dggngvcv
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3001 tegkryriyh latsksksks eraniqlaat kktqyqqlpv sdeilfqiyy preplhfskf
3061 ldpdfqpscs evdligfvvs vvkktglapf vylsdecynl laikfwidln ediikphmli
3121 aasnlqwrpe sksglltlfa gdfsvfsasp keghfgetfn kmkntvenid ilcneaenkl
3181 mhlhandpk wstptkdcts gpytaqiipg tgnkllmssp nceiyyqspl slcmakrksv
3241 stpvsaqmts ksckgekeid dqknckkrra ldflsrlplp ppvspictfv spaaqkafqp
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3361 qfisvsestr taptssedyl rlkrrcttsl ikeqessgas teeceknkqd titttkkyi

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☐ 1: AAA43099. Reports hemagglutinin [In...[gi:323995]BLink, Conserved
Domains, LinksFeatures Sequence

LOCUS AAA43099 566 aa linear VRL 13-JUL-2006
 DEFINITION hemagglutinin [Influenza A virus (A/Udorn/307/1972 (H3H2))].
 ACCESSION AAA43099
 VERSION AAA43099.1 GI:323995
 DBSOURCE locus FLADORNHA accession M54895.1
 KEYWORDS
 SOURCE Influenza A virus (A/Udorn/307/1972 (H3H2))
 ORGANISM Influenza A virus (A/Udorn/307/1972 (H3H2))
 Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 Influenzavirus A.
 REFERENCE 1 (residues 1 to 566)
 AUTHORS Iuferov, V.P., Karginov, V.A., Samokhvalov, E.I., Chizhikov, V.E. and
 Vasilenko, S.K.
 TITLE Nucleotide sequence of the hemagglutinin gene of the influenza
 virus A/Udorn/307/72 (H3N2)
 JOURNAL Dokl. Akad. Nauk SSSR 278 (3), 738-742 (1984)
 PUBMED 6548691
 COMMENT Method: conceptual translation.
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ORIGIN

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121 yaslrslvas sgtlefiseg ftwtgvtqng gsnackrgpd sgffsrlnwl yksgstypvl
181 nvtmpnndnf dklyiwgvhh pstdqeqtsl yvqasgrvtv stkrsqqtii pnigsrpwvr
241 glssrisiyw tivkpgdilv insngnliap rgyfkmrtgk ssimrsdapi gtcisecitp
301 ngsipndkpf qnvnkitxga cpkyvkqntl klatgmrnvp ekqtrglfsa iagfiengwe
361 gmidgwygfr hqnsegtgqp adlkstqaai dqingklnrv iektnekfhq iekefseveg
421 riqdlekyve dtkidlwsyn aellvalenq htidltdsem nklfektsrq lrenaedmgn
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541 fllcvllgf imtacqkgni rcnici
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